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(54) Title: NUCLEIC ACID METHYLATION DETECTION PROCESS USING AN INTERNAL REFERENCE SAMPLE

(57) Abstract: There is disclosed a process for detection of DNA methylation at CpG sites using nucleic acid arrays and preferably microarrays. Specifically, there is disclosed a process for directly generating a reference sample from the sample to be tested and detecting methylation at large numbers of CpG island sites simultaneously. More specifically, the inventive process comprises dividing a DNA sample into two samples (a first sample and a second sample), amplifying the first DNA sample by a nucleic acid amplification process such that any methylcytosine residues are amplified as unmethylated cytosine residues, treating the amplified first sample and the (unamplified) second sample with bisulfite to convert unmethylated cytosine residues in both samples to deoxyuracil residues, labeling the bisulfite-converted second sample with a second fluorescent marker and the bisulfite-converted first sample with a first fluorescent marker, wherein the first and second fluorescent markers have non-overlapping fluorescent excitation and emission spectra; and hybridizing the first sample and the second sample onto a microarray device having a plurality of oligonucleotide capture probes designed to hybridize to CpG island sites of the DNA sample as converted and non-converted by bisulfite.



WO 2004/059007 A2